FIG. 1

```
          ccggaattcccgggtcgacccacgcgtccggccccccattcaagaagccgctcagctatcccggccagcacagggcgc
          ccggcgcgcctcggagcgcaagttcctcgccttctcctgcccgctcgctgggcattatgcggccaagcagccgagccccagtcctc
  5       ctcctcctcctgctcctccggctcctcctgcggcccgagcggctcagctctcggcaggcggcggcgttgctcagccgagcgcagac
          gggaccctcgcagcgagacctcagcgactcctaaagtcaaaagttggcggcgggcgccgggctccgcgcgctctccacggccgctg
          cctcgcgtcgccgccgcagccaaggagggcaggaggaggggggtgggggcagcggaggagggggtgggaagcaccatgcagtttg
          tatcctgggccacactgctaacgctcctggtgcgggacctggccgagatggggagcccagacgccgcggcggccgtgcgcaaggac
          aggctgcacccgaggcaagtgaaattattagagaccctgagcgaatacgaaatcgtgtctcccatccgagtgaacgctctcggaga
  10      accctttcccacgaacgtccacttcaaaagaacgcgacggagcattaactctgccactgaccctggcctgccttcgcctcctcct
          cttcctcctctacctcctcccaggcgcattaccgcctctctgccttcggccagcagtttctatttaatctcaccgccaatgccgga
          tttatcgctccactgttcactgtcaccctcctcgggacgcccggggtgaatcagaccaagtttattccgaagaggaagcggaact
          caagcactgtttctacaaaggctatgtcaataccaactccgagcacacggccgtcatcagcctctgctcaggaatgctgggcacat
          tccggtctcatgatggggattatttttattgaaccactacagtctatggatgaacaagaagatgaagaggaacaaaacaaacccac
  15      atcatttataggcgcagcgcccccagagagagccctcaacaggaaggcatgcatgtgacacctcagaacacaaaaataggcacag
          taaagacaagaagaaaaccagagcaagaaaatggggagaaaggattaacctggctggtgacgtagcagcattaaacagcggcttag
          caacagaggcattttctgcttatggtaataagacggacaacacaagagaaaagaggacccacagaaggacaaaacgttttttatcc
          tatccacggtttgtagaagtcttggtggtggcagacaacagaatggtttcataccatggagaaaaaccttcaacactatattttaac
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  20      ataatgaacaggatgggccttccatatcttttaatgctcagacaacattaaaaaacttttgccagtggcagcattcgaagaacagt
          ccaggtggaatccatcatgatactgctgttctcttaacaagacaggatatctgcagagctcacgacaaatgtgataccttaggcct
          ggctgaactgggaaccatttgtgatccctatagaagctgttctattagtgaagatagtggattgagtacagcttttacgatcgccc
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          gctccaacactgaacttctacaccaacccctggatgtggtcaaagtgtagtcgaaaatatatcactgagttttttagacactggtta
  25      tggcgagtgtttgcttaacgaacctgaatccagaccctacccctttgcctgtccaactgccaggcatcctttacaacgtgaataaac
          aatgtgaattgattttttggaccaggttctcaggtgtgcccatatatgatgcagtgcagacggctctggtgcaataacgtcaatgga
          gtacacaaaggctgccggactcagcacacaccctgggccgatgggacggagtgcgagcctggaaagcactgcaagtatggattttg
          tgttcccaaagaaatggatgtccccgtgacagatggatcctggggaagttggagtcccctttggaacctgctccagaacatgtggag
          ggggcatcaaaacagccattcgagagtgcaacagaccagaaccaaaaaatggtggaaaatactgtgtaggacgtagaatgaaattt
  30      aagtcctgcaacacggagccatgtctcaagcagaagcgagacttccgagatgaacagtgtgctcactttgacgggaagcattttaa
          catcaacggtctgcttcccaatgtgcgctgggtccctaaatacagtggaattctgatgaaggaccggtgcaagttgttctgcagag
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          cagggcctttgccggcaagctggatgcgatcatgtttttaaactcaaaagcccggagagataaatgtggggtttgtggtggcgataa
          ttcttcatgcaaaacagtggcaggaacatttaatacagtacattatggttacaatactgtggtccgaattccagctggtgctacca
  35      atattgatgtgcggcagcacagtttctcaggggaaacagacgatgacaactacttagctttatcaagcagtaaaggtgaattcttg
          ctaaatggaaactttgttgtcacaatggccaaaagggaaattcgcattgggaatgctgtggtagagtacagtgggtccgagactgc
          cgtagaaagaattaactcaacagatcgcattgagcaagaacttttgcttcaggtttttgtcggtgggaaagttgtacaaccccgatg
          tacgctattctttcaatattccaattgaagataaacctcagcagttttactggaacagtcatgggccatggcaagcatgcagtaaa
          ccctgccaaggggaacggaaacgaaaacttgtttgcaccagggaatctgatcagcttactgtttctgatcaaagatgcgatcggct
  40      gccccagcctggacacattactgaaccctgtggtacagactgtgacctgaggtggcatgttgccagcaggagtgaatgtagtgccc
          agtgtggcttgggttaccgcacattggacatctactgtgccaaatatagcaggctggatgggaagactgagaaggttgatgatggt
          ttttgcagcagccatcccaaaccaagcaaccgtgaaaaatgctcaggggaatgtaacacgggtggctggcgctattctgcctggac
          tgaatgttcaaaaagctgtgacggtgggacccagaggagaagggctatttgtgtcaataccgaaatgatgtactggatgacagca
          aatgcacacatcaagagaaagttaccattcagaggtgcagtgagttcccttgtccacagtggaaatctggagactggtcagagtgc
  45      ttggtcacctgtggaaaagggcataagcaccgccaggtctggtgtcagtttggtgaagatcgattaaatgatagaatgtgtgtgaccc
```

tgagaccaagccaacatctatgcagacttgtcagcagccggaatgtgcatcctggcaggcgggtccctggggacagtgcagtgtca
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ggaggaagatgcccccaaatggaaagctggcgcttggagtcagtgctctgtgtcctgtggccgaggcgtacagcagaggcatgtggg
ctgtcagatcggaacacacaaaatagccagagagaccgagtgcaacccatacaccagaccggagtcggaacgcgactgccaaggcc
cacggtgtcccctctacacttggagggcagaggaatggcaagaatgcaccaagacctgcggcgaaggctccaggtaccgcaaggtg
gtgtgtgtggatgacaacaaaaacgaggtgcatggggcacgctgtgacgtgagcaagcggccggtggaccgtgaaagctgtagttt
gcaaccctgcgagtatgtctggatcacaggagaatggtcagaggtaccgtcctgggaactgtaaccatcgtcagctcagccatggc
ctgagagtggcagagggatgagtggagggatgagtgcaggaatgtgggagacttgaggctacccgcccgatttgccactgtgaact
gtgtgtttctgacaagtcctcagctttcccaagctagaattccttgtatgcaaagcgggagagatgtaagagatggtctctaagt
cccttcaggtctacattctgtgattcaccttgatgtcctattggcataaagaagaaattattacaggggctgcaaactcataggat
gctgtgaggtgcctgaagacagttaagtataagaaaatattgtagtgccaggatacaacaaggagagatggcaactgtgacaaac
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ttttcaagagaggctaaaaatctggactagtatgtgagatttcctaacttgaaaatggggctgaaattttttggttttaaaacatt
gtaaggggcaaacaaaccccctttcatgaaccagatgtgttgtgcctgtttaacaaacagcttcagaggaagaaaataattttctat
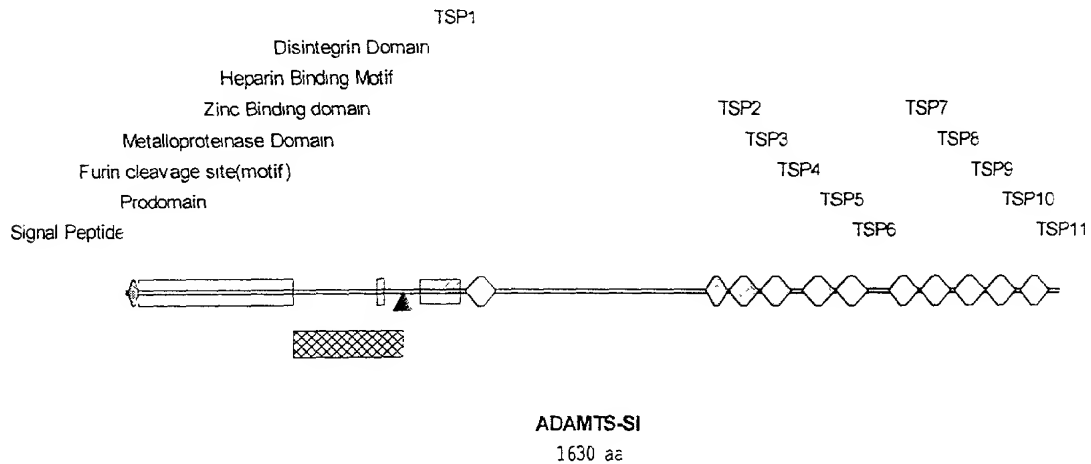aatatccgaagtatctcaagtac

FIG. 2

```
        mqfvswatlltllvrdlaemgspdaaaavrkdrlhprqvklletlseyeivspirvnalgepfptnvhfkrtrrsıns
    atdpwpafassssssstssqahyrlsafgqqflfnltanagfiaplftvtllgtpgvnqtkfyseeeaelkhcfykgyvntnsehta
    vislcsgmlgtfrshdgdyfıeplqsmdeqedeeeqnkphiiyrrsapqrepstgrhacdtsehknrhskdkkktrarkwgerinl
    agdvaalnsglateafsaygnktdntrekrthrrtkrflsyprfvevlvvadnrmvsyhgenlqhyiltlmsivasiykdpsignl
    inivivnlivihneqdgpsisfnaqttlknfcqwqhsknspggihhdtavlltrqdicrahdkcdtlglaelgticdpyrscsise
    dsglstaftıahelghvfnmphddnnkckeegvkspqhvmaptlnfytnpwmwskcsrkyitefldtgygecllnepesrpyplpv
    qlpgilynvnkqcelifgpgsqvcpymmqcrrlwcnnvngvhkgcrtqhtpwadgtecepgkhckygfcvpkemdvpvtdgswgsw
    spfgtcsrtcgggiktaırecnrpepknggkycvgrrmkfkscntepclkqkrdfrdeqcahfdgkhfningllpnvrwvpkysgi
    lmkdrcklfcrvagntayyqlrdrvidgtpcgqdtndicvqglcrqagcdhvlnskarrdkcgvcggdnsscktvagtfntvhygy
    ntvvripagatnidvrqhsfsgetdddnylalsssskgefllngnfvvtmakreirignavveysgsetaverinstdrieqelllq
    vlsvgklynpdvrysfnıpiedkpqqfywnshgpwqacskpcqgerkrklvctresdqltvsdqrcdrlpqpghitepcgtdcdlr
    whvasrsecsaqcglgyrtldiycakysrldgktekvddgfcsshpkpsnrekcsgecntggwrysawtecskscdggtqrrraıc
    vntrndvlddskcthqekvtiqrcsefpcpqwksgdwseclvtcgkghkhrqvwcqfgedrlndrmcdpetkptsmqtcqqpecas
    wqagpwgqcsvtcgqgyqlravkciigtymsvvddndcnaatrptdtqdcelpschpppaapetrrstysaprtqwrfgswtpcsa
    tcgkgtrmryvscrdengsvadesacatlprpvakeecsvtpcgqwkaldwsscsvtcgqgratrqvmcvnysdhvidrsecdqdy
    ipetdqdcsmspcpqrtpdsglaqhpfqnedyrprsaspsrthvlggnqwrtgpwgacsstcaggsqrrvvvcqdengytandcve
    rikpdeqracesgpcpqwaygnwgectklcgggirtrlvvcqrsngerfpdlsceildkppdreqcnthacphdaawstgpwsscs
    vscgrghkqrnvycmakdgshlesdyckhlakphghrkcrggrcpkwkagawsqcsvscgrgvqqrhvgcqigthkiaretecnpy
    trpeserdcqgprcplytwraeewqectktcgegsryrkvvcvddnknevhgarcdvskrpvdrescslqpceyvwitgewsevps
    wel*
```

Fig. 3

Domain structure of ADAMTS-SI

Signal peptide (1-18), Prodomain (19-287), Furin cleavage site (288),
Metalloproteinase domain (289-478), Zinc binding motif (434-446),
Heparin binding motif (478-482), Disintegrin domain (509-578),
Thrombospondin motif (589-642), Spacer region (643-1014),
Thrombospondin submotifs (1001-1053, 1056-1108, 1111-1165, 1186-1239,
1240-1295, 1332-1383, 1386-1439,1445-1500, 1501-1554, 1559-1612)

ADAMTS-SI
1630 aa

1   CCGGAATTCC CGGGTCGACC CACGCGTCCG GCCCCCCATT CAAGAAGCCG CTCAGCTATC
    GGCCTTAAGG GCCCAGCTGG GTGCGCAGGC CGGGGGGTAA GTTCTTCGGC GAGTCGATAG

61 CCGGCCAGCA CAGGGCGCCC GGCGCGCCTC GGAGCGCAAG TTCCTCGCCT TCTCCTGCCC
    GGCCGGTCGT GTCCCGCGGG CCGCGCGGAG CCTCGCGTTC AAGGAGCGGA AGAGGACGGG

121 GCTCGCTGGG CATTATGCGG CCAAGCAGCC GAGCCCCAGT CCTCCTCCTC CTCCTGCTCC
    CGAGCGACCC GTAATACGCC GGTTCGTCGG CTCGGGGTCA GGAGGAGGAG GAGGACGAGG

181 TCCGGCTCCT CCTGCGGCCC GAGCGGCTCA GCTCTCGGCA GGCGGCGGCC TTGCTCAGCC
    AGGCCGAGGA GGACGCCGGG CTCGCCGAGT CGAGAGCCGT CCGCCGCCGC AACGAGTCGG

241 GAGCGCAGAC GGGACCCTCG CAGCGAGACC TCAGCGACTC CTAAAGTCAA AAGTTGGCGG
    CTCGCGTCTG CCCTGGGAGC GTCGCTCTGG AGTCGCTGAG GATTTCAGTT TTCAACCGCC

301 CGGGCGCCGG GCTCCGCGCG CTCTCCACGG CCGCTGCCTC GCGTCGCCGC CGCAGCCAAG
    GCCCGCGGCC CGAGGCGCGC GAGAGGTGCC GGCGACGGAG CGCAGCGGCG CGTCGGTTC

                                                        M   Q   F
                                                   Start met
                                                        = = =
                                                   Kozak consensus
                                                   = = = = = = =
                                                   Signal peptide
                                                   = = = = = = =
361 GAGGGCAGGA GGGAGGGGGG TGGGGGCAGC GGAGGGAGGG GTGGGAAGCA CCATGCAGTT
    CTCCCGTCCT CCCTCCCCCC ACCCCCGTCG CCTCCCTCCC CACCCTTCGT GGTACGTCAA

+2   V   S   W   A   T   L   L   T   L   L   V   R   D   L   A   E   M   G   S   P
                                              signal peptide cleavage site
                                                        =
             Signal peptide   Prodomain
      = = = = = = = = = = = = =
421 TGTATCCTGG GCCACACTGC TAACGCTCCT GGTGCGGGAC CTGGCCGAGA TGGGGAGCCC
    ACATAGGACC CGGTGTGACG ATTGCGAGGA CCACGCCCTG GACCGGCTCT ACCCCTCGGG

+2   D   A   A   A   A   V   R   K   D   R   L   H   P   R   Q   V   K   L   L   E
                                                             Prodomain
      =
481 AGACGCCGCG GCGGCCGTGC GCAAGGACAG GCTGCACCCG AGGCAAGTGA AATTATTAGA
    TCTGCGGCGC CGCCGGCACG CGTTCCTGTC CGACGTGGGC TCCGTTCACT TTAATAATCT

+2   T   L   S   E   Y   E   I   V   S   P   I   R   V   N   A   L   G   E   P   F
                                                             Prodomain
      =
541 GACCCTGAGC GAATACGAAA TCGTGTCTCC CATCCGAGTG AACGCTCTCG GAGAACCCTT
    CTGGGACTCG CTTATGCTTT AGCACAGAGG GTAGGCTCAC TTGCGAGAGC CTCTTGGGAA

+2   P   T   N   V   H   F   K   R   T   R   R   S   I   N   S   A   T   D   P   W
                                                             Prodomain
      =
601 TCCCACGAAC GTCCACTTCA AAAGAACGCG ACGGAGCATT AACTCTGCCA CTGACCCCTG

```
 +2    P   A   F    A   S   S   S    S   S   S    T   S   S    Q   A   H   Y    R   L   S
                                                                          Prodomain
       ============================================================================
 661   GCCTGCCTTC  GCCTCCTCCT  CTTCCTCCTC  TACCTCCTCC  CAGGCGCATT  ACCGCCTCTC
       CGGACGGAAG  CGGAGGAGGA  GAAGGAGGAG  ATGGAGGAGG  GTCCGCGTAA  TGGCGGAGAG

 +2     A   F   G    Q   Q   F   L    F   N   L    T   A   N    A   G   F   I    A   P   L
                                                                          Prodomain
       ============================================================================
 721   TGCCTTCGGC  CAGCAGTTTC  TATTTAATCT  CACCGCCAAT  GCCGGATTTA  TCGCTCCACT
       ACGGAAGCCG  GTCGTCAAAG  ATAAATTAGA  GTGGCGGTTA  CGGCCTAAAT  AGCGAGGTGA

 +2     F   T   V    T   L   L   G    T   P   G    V   N   Q    T   K   F   Y    S   E   E
                                                                          Prodomain
       ============================================================================
 781   GTTCACTGTC  ACCCTCCTCG  GGACGCCCGG  GGTGAATCAG  ACCAAGTTTT  ATTCCGAAGA
       CAAGTGACAG  TGGGAGGAGC  CCTGCGGGCC  CCACTTAGTC  TGGTTCAAAA  TAAGGCTTCT

 +2     E   A   E    L   K   H   C    F   Y   K    G   Y   V    N   T   N   S    E   H   T
                                         Prodomain
       ============================================================================
 841   GGAAGCGGAA  CTCAAGCACT  GTTTCTACAA  AGGCTATGTC  AATACCAACT  CCGAGCACAC
       CCTTCGCCTT  GAGTTCGTGA  CAAAGATGTT  TCCGATACAG  TTATGGTTGA  GGCTCGTGTG

 +2     A   V   I    S   L   C   S    G   M   L    G   T   F    R   S   H   D    G   D   Y
       Prodomain
       ============================================================================
 901   GGCCGTCATC  AGCCTCTGCT  CAGGAATGCT  GGGCACATTC  CGGTCTCATG  ATGGGGATTA
       CCGGCAGTAG  TCGGAGACGA  GTCCTTACGA  CCCGTGTAAG  GCCAGAGTAC  TACCCCTAAT

 +2     F   I   E    P   L   Q   S    M   D   E    Q   E   D    E   E   E   Q    N   K   P
       Prodomain
       ============================================================================
 961   TTTTATTGAA  CCACTACAGT  CTATGGATGA  ACAAGAAGAT  GAAGAGGAAC  AAAACAAACC
       AAAATAACTT  GGTGATGTCA  GATACCTACT  TGTTCTTCTA  CTTCTCCTTG  TTTTGTTTGG

 +2     H   I   I    Y   R   R   S    A   P   Q    R   E   P    S   T   G   R    H   A   C
       Prodomain
       ============================================================================
1021   CCACATCATT  TATAGGCGCA  GCGCCCCCCA  GAGAGAGCCC  TCAACAGGAA  GGCATGCATG
       GGTGTAGTAA  ATATCCGCGT  CGCGGGGGGT  CTCTCTCGGG  AGTTGTCCTT  CCGTACGTAC

 +2     D   T   S    E   H   K   N    R   H   S    K   D   K    K   K   T   R    A   R   K
       Prodomain
       ============================================================================
1081   TGACACCTCA  GAACACAAAA  ATAGGCACAG  TAAAGACAAG  AAGAAAACCA  GAGCAAGAAA
       ACTGTGGAGT  CTTGTGTTTT  TATCCGTGTC  ATTTCTGTTC  TTCTTTTGGT  CTCGTTCTTT

 +2     W   G   E    R   I   N   L    A   G   D    V   A   A    L   N   S   G    L   A   T
       Prodomain
       ============================================================================
1141   ATGGGGAGAA  AGGATTAACC  TGGCTGGTGA  CGTAGCAGCA  TTAAACAGCG  GCTTAGCAAC
       TACCCCTCTT  TCCTAATTGG  ACCGACCACT  GCATCGTCGT  AATTTGTCGC  CGAATCGTTG
```

```
 -2    E   A  F   S   A   Y   G   N   K   T   D   N   T   R   E   K   R   T   H   F
       Prodomain.
       ============================================================================
 1201  AGAGGCATTT TCTGCTTATG GTAATAAGAC GGACAACACA AGAGAAAAGA GGACCCACAG
       TCTCCGTAAA AGACGAATAC CATTATTCTG CCTGTTGTGT TCTCTTTTCT CCTGGGTGTC


  +2    R   T   K   R   F   L   S   Y   P   F   V   E   V   L   V   V   A   D   N
       Furin Cleavage  site

                            =

       Prodomain.                                 Metalloproteinase   domain
       ============================================================================
 1261  AAGGACAAAA CGTTTTTTAT CCTATCCACG GTTTGTAGAA GTCTTGGTGG TGGCAGACAA
       TTCCTGTTTT GCAAAAAATA GGATAGGTGC CAAACATCTT CAGAACCACC ACCGTCTGTT


  +2    R   M   V   S   Y   H   G   E   N   L   Q   H   Y   I   L   T   L   M   S   I
                                            Metalloproteinase   domain
       ============================================================================
 1321  CAGAATGGTT TCATACCATG GAGAAAACCT TCAACACTAT ATTTTAACTT TAATGTCAAT
       GTCTTACCAA AGTATGGTAC CTCTTTTGGA AGTTGTGATA TAAAATTGAA ATTACAGTTA


  +2    V   A   S   I   Y   K   D   P   S   I   G   N   L   I   N   I   V   I   V   N
                                            Metalloproteinase   domain
       ============================================================================
 1381  TGTAGCCTCT ATCTATAAAG ACCCAAGTAT TGGAAATTTA ATTAATATTG TTATTGTGAA
       ACATCGGAGA TAGATATTTC TGGGTTCATA ACCTTTAAAT TAATTATAAC AATAACACTT


  +2    L   I   V   I   H   N   E   Q   D   G   P   S   I   S   F   N   A   Q   T   T
                                            Metalloproteinase   domain
       ============================================================================
 1441  CTTAATTGTG ATTCATAATG AACAGGATGG GCCTTCCATA TCTTTTAATG CTCAGACAAC
       GAATTAACAC TAAGTATTAC TTGTCCTACC CGGAAGGTAT AGAAAATTAC GAGTCTGTTG


  +2    L   K   N   F   C   Q   W   Q   H   S   K   N   S   P   G   G   I   H   H   D
                                            Metalloproteinase   domain
       ============================================================================
 1501  ATTAAAAAAC TTTTGCCAGT GGCAGCATTC GAAGAACAGT CCAGGTGGAA TCCATCATGA
       TAATTTTTTG AAAACGGTCA CCGTCGTAAG CTTCTTGTCA GGTCCACCTT AGGTAGTACT


  +2    T   A   V   L   L   T   R   Q   D   I   C   R   A   H   D   K   C   D   T   I
       Metalloproteinase domain
       ============================================================================
 1561  TACTGCTGTT CTCTTAACAA GACAGGATAT CTGCAGAGCT CACGACAAAT GTGATACCTT
       ATGACGACAA GAGAATTGTT CTGTCCTATA GACGTCTCGA GTGCTGTTTA CACTATGGAA


  +2    G   L   A   E   L   G   T   I   C   D   P   Y   R   S   C   S   I   S   E   D
       Metalloproteinase domain
       ============================================================================
 1621  AGGCCTGGCT GAACTGGGAA CCATTTGTGA TCCCTATAGA AGCTGTTCTA TTAGTGAAGA
       TCCGGACCGA CTTGACCCTT GGTAAACACT AGGGATATCT TCGACAAGAT AATCACTTCT
```

```
+2   S  G  L   S  T  A  F   T  I  A   H  E  L   G  H  V  F   N  M  P
                                              Zinc Binding  Domain

                                ===================================
     Metalloproteinase  domain
     ==============================================================
1681 TAGTGGATTG AGTACAGCTT TTACGATCGC CCATGAGCTG GGCCATGTGT TTAACATGCC
     ATCACCTAAC TCATGTCGAA AATGCTAGCG GGTACTCGAC CCGGTACACA AATTGTACGG


  +2    H  D  D   N  N  K  C   K  E  E   G  V  K   S  P  Q  H   V  M  A
     Zinc Binding  Domain
     ==========
     Metalloproteinase  domain
     ==============================================================
1741 TCATGATGAC AACAACAAAT GTAAAGAAGA AGGAGTTAAG AGTCCCCAGC ATGTCATGGC
     AGTACTACTG TTGTTGTTTA CATTTCTTCT TCCTCAATTC TCAGGGGTCG TACAGTACCG


   +2   P  T  L   N  F  Y  T   N  P  W   M  W  S   K  C  S  R   K  Y  I
                                   Heparin Binding  Motif
                                   ==============
     Metalloproteinase  domain                     Heparin  Binding  Motif
     =========================                     ================
1801 TCCAACACTG AACTTCTACA CCAACCCCTG GATGTGGTCA AAGTGTAGTC GAAAATATAT
     AGGTTGTGAC TTGAAGATGT GGTTGGGGAC CTACACCAGT TTCACATCAG CTTTTATATA


   +2   T  E  F   L  D  T  G   Y  G  E   C  L  L   N  E  P   E   S  R  P
1861 CACTGAGTTT TTAGACACTG GTTATGGCGA GTGTTTGCTT AACGAACCTG AATCCAGACC
     GTGACTCAAA AATCTGTGAC CAATACCGCT CACAAACGAA TTGCTTGGAC TTAGGTCTGG


   +2   Y  P  L   P  V  Q  L   P  G  I   L  Y  N   V  N  K  Q   C  E  L
                                                 Disintegrin  domain
                                ===================================
1921 CTACCCTTTG CCTGTCCAAC TGCCAGGCAT CCTTTACAAC GTGAATAAAC AATGTGAATT
     GATGGGAAAC GGACAGGTTG ACGGTCCGTA GGAAATGTTG CACTTATTTG TTACACTTAA


   +2   I  F  G   P  G  S  Q   V  C  P   Y  M  M   Q  C  R  R   L  W  C
                                                 Disintegrin  domain
     ==============================================================
1981 GATTTTTGGA CCAGGTTCTC AGGTGTGCCC ATATATGATG CAGTGCAGAC GGCTCTGGTG
     CTAAAAACCT GGTCCAAGAG TCCACACGGG TATATACTAC GTCACGTCTG CCGAGACCAC


   +2   N  N  V   N  G  V  H   K  G  C   R  T  Q   H  T  P  W   A  D  G
                 Disintegrin   domain
     ==============================================================
2041 CAATAACGTC AATGGAGTAC ACAAAGGCTG CCGGACTCAG CACACACCCT GGGCCGATGG
     GTTATTGCAG TTACCTCATG TGTTTCCGAC GGCCTGAGTC GTGTGTGGGA CCCGGCTACC


   +2   T  E  C   E  P  G  K   H  C  K   Y  G  F   C  V  P  K   E  M  D
     Disintegrin  domain
     ==============================================================
2101 GACGGAGTGC GAGCCTGGAA AGCACTGCAA GTATGGATTT TGTGTTCCCA AAGAAATGGA
     CTGCCTCACG CTCGGACCTT TCGTGACGTT CATACCTAAA ACACAAGGGT TTCTTTACCT
```

```
 -:         V  P  V   T  D  G  S   W  G  S   W  S  F   F  G  T  C   S  R  T
            Disintegrin domain                                        TSP1
            =================     ===========================================
      2161  TGTCCCCGTG ACAGATGGAT CCTGGGGAAG TTGGAGTCCC TTTGGAACCT GCTCCAGAAC
            ACAGGGGCAC TGTCTACCTA GGACCCCTTC AACCTCAGGG AAACCTTGGA CGAGGTCTTG


       +2   C  G  G   G  I  K  T   A  I  R   E  C  N   R  P  E  F   K  N  G
                                                 TSP1
            ==========================================================================
      2221  ATGTGGAGGG GGCATCAAAA CAGCCATTCG AGAGTGCAAC AGACCAGAAC CAAAAAATGG
            TACACCTCCC CCGTAGTTTT GTCGGTAAGC TCTCACGTTG TCTGGTCTTG GTTTTTTACC


       +2   G  K  Y   C  V  G  R   R  M  K   F  K  S   C  N  T  E   P  C  L
            TSP1                                                Spacer Region
            ==========================================================================
      2281  TGGAAAATAC TGTGTAGGAC GTAGAATGAA ATTTAAGTCC TGCAACACGG AGCCATGTCT
            ACCTTTTATG ACACATCCTG CATCTTACTT TAAATTCAGG ACGTTGTGCC TCGGTACAGA


       +2   K  Q  K   R  D  F  R   D  E  Q   C  A  H   F  D  G  K   H  F  N
                                                                Spacer Region
            ==========================================================================
      2341  CAAGCAGAAG CGAGACTTCC GAGATGAACA GTGTGCTCAC TTTGACGGGA AGCATTTTAA
            GTTCGTCTTC GCTCTGAAGG CTCTACTTGT CACACGAGTG AAACTGCCCT TCGTAAAATT


       +2   I  N  G   L  L  P  N   V  R  W   V  P  K   Y  S  G  I   L  M  K
                                                                Spacer Region
            ==========================================================================
      2401  CATCAACGGT CTGCTTCCCA ATGTGCGCTG GGTCCCTAAA TACAGTGGAA TTCTGATGAA
            GTAGTTGCCA GACGAAGGGT TACACGCGAC CCAGGGATTT ATGTCACCTT AAGACTACTT


       +2   D  R  C   K  L  F  C   R  V  A   G  N  T   A  Y  Y  Q   L  R  D
                                                                Spacer Region
            ==========================================================================
      2461  GGACCGGTGC AAGTTGTTCT GCAGAGTGGC AGGGAACACA GCCTACTATC AGCTTCGAGA
            CCTGGCCACG TTCAACAAGA CGTCTCACCG TCCCTTGTGT CGGATGATAG TCGAAGCTCT


       +2   R  V  I   D  G  T  P   C  G  Q   D  T  N   D  I  C  V   Q  G  L
                                                                Spacer Region
            ==========================================================================
      2521  CAGAGTGATA GATGGAACTC CTTGTGGCCA GGACACAAAT GATATCTGTG TCCAGGGCCT
            GTCTCACTAT CTACCTTGAG GAACACCGGT CCTGTGTTTA CTATAGACAC AGGTCCCGGA


       +2   C  R  Q   A  G  C  D   H  V  L   N  S  K   A  R  R  D   K  C  G
                                                                Spacer Region
            ==========================================================================
      2581  TTGCCGGCAA GCTGGATGCG ATCATGTTTT AAACTCAAAA GCCCGGAGAG ATAAATGTGG
            AACGGCCGTT CGACCTACGC TAGTACAAAA TTTGAGTTTT CGGGCCTCTC TATTTACACC


       +2   V  C  G   G  D  N  S   S  C  K   T  V  A   G  T  F  N   T  V  H
                                                                Spacer Region
            ==========================================================================
      2641  GGTTTGTGGT GGCGATAATT CTTCATGCAA AACAGTGGCA GGAACATTTA ATACAGTACA
            CCAAACACCA CCGCTATTAA GAAGTACGTT TTGTCACCGT CCTTGTAAAT TATGTCATGT
```

```
  +2   Y  G  Y   N  T  V  V   R  I  F   A  G  A   T  N  I  D   V  R  C
                                                      Spacer  Region
       =================================================================
 2701  TTATGGTTAC AATACTGTGG TCCGAATTCC AGCTGGTGCT ACCAATATTG ATGTGCGGCA
        AATACCAATG TTATGACACC AGGCTTAAGG TCGACCACGA TGGTTATAAC TACACGCCGT


  +2   H  S  F   S  G  E  T   D  D  D   N  Y  L   A  L  S  S   S  K  G
                                                      Spacer  Region
       =================================================================
 2761  GCACAGTTTC TCAGGGGAAA CAGACGATGA CAACTACTTA GCTTTATCAA GCAGTAAAGG
        CGTGTCAAAG AGTCCCCTTT GTCTGCTACT GTTGATGAAT CGAAATAGTT CGTCATTTCC


  +2   E  F  L   L  N  G  N   F  V  V   T  M  A   K  R  E  I   R  I  G
                                                      Spacer  Region
       =================================================================
 2821  TGAATTCTTG CTAAATGGAA ACTTTGTTGT CACAATGGCC AAAAGGGAAA TTCGCATTGG
        ACTTAAGAAC GATTTACCTT TGAAACAACA GTGTTACCGG TTTTCCCTTT AAGCGTAACC


  +2   N  A  V   V  E  Y  S   G  S  E   T  A  V   E  R  I  N   S  T  D
                 Spacer Region
       =================================================================
 2881  GAATGCTGTG GTAGAGTACA GTGGGTCCGA GACTGCCGTA GAAAGAATTA ACTCAACAGA
        CTTACGACAC CATCTCATGT CACCCAGGCT CTGACGGCAT CTTTCTTAAT TGAGTTGTCT


  +2   R  I  E   Q  E  L  L   L  Q  V   L  S  V   G  K  L  Y   N  P  D
       Spacer Region
       =================================================================
 2941  TCGCATTGAG CAAGAACTTT TGCTTCAGGT TTTGTCGGTG GGAAAGTTGT ACAACCCCGA
        AGCGTAACTC GTTCTTGAAA ACGAAGTCCA AAACAGCCAC CCTTTCAACA TGTTGGGGCT


  +2   V  R  Y   S  F  N  I   P  I  E   D  K  P   Q  Q  F  Y   W  N  S
       Spacer Region
       =================================================================
 3001  TGTACGCTAT TCTTTCAATA TTCCAATTGA AGATAAACCT CAGCAGTTTT ACTGGAACAG
        ACATGCGATA AGAAAGTTAT AAGGTTAACT TCTATTTGGA GTCGTCAAAA TGACCTTGTC


  +2   H  G  P   W  Q  A  C   S  K  P   C  Q  G   E  R  K  R   K  L  V
       Spacer Region
       =================================================================
 3061  TCATGGGCCA TGGCAAGCAT GCAGTAAACC CTGCCAAGGG AACGGAAAC GAAAACTTGT
        AGTACCCGGT ACCGTTCGTA CGTCATTTGG GACGGTTCCC CTTGCCTTTG CTTTTGAACA


  +2   C  T  R   E  S  D  Q   L  T  V   S  D  Q   R  C  D  R   L  P  C
       Spacer Region
       =================================================================
 3121  TTGCACCAGG GAATCTGATC AGCTTACTGT TTCTGATCAA AGATGCGATC GGCTGCCCCA
        AACGTGGTCC CTTAGACTAG TCGAATGACA AAGACTAGTT TCTACGCTAG CCGACGGGGT


  +2   P  G  H   I  T  E  P   C  G  T   D  C  D   L  R  W  H   V  A  S
       Spacer Region
       =================================================================
 3181  GCCTGGACAC ATTACTGAAC CCTGTGGTAC AGACTGTGAC CTGAGGTGGC ATGTTGCCAG
        CGGACCTGTG TAATGACTTG GGACACCATG TCTGACACTG GACTCCACCG TACAACGGTC
```

```
  +2    R   S   E   C   S   A   Q   C   G   L   G   Y   R   T   L   D   I   Y   C   A
     Spacer Region

     =======================================================================
3241 CAGGAGTGAA TGTAGTGCCC AGTGTGGCTT GGGTTACCGC ACATTGGACA TCTACTGTGC
     GTCCTCACTT ACATCACGGG TCACACCGAA CCCAATGGCG TGTAACCTGT AGATGACACG


  +2    K   Y   S   R   L   D   G   K   T   E   K   V   D   D   G   F   C   S   S   H
     Spacer Region

     =======================================================================
3301 CAAATATAGC AGGCTGGATG GGAAGACTGA GAAGGTTGAT GATGGTTTTT GCAGCAGCCA
     GTTTATATCG TCCGACCTAC CCTTCTGACT CTTCCAACTA CTACCAAAAA CGTCGTCGGT


  +2    P   K   F   S   N   R   E   K   C   S   G   E   C   N   T   G   G   W   R   Y
     Spacer Region

     =======================================================================
3361 TCCCAAACCA AGCAACCGTG AAAAATGCTC AGGGGAATGT AACACGGGTG CTGGCGCTA
     AGGGTTTGGT TCGTTGGCAC TTTTTACGAG TCCCCTTACA TTGTGCCCAC CGACCGCGAT


  +2    S   A   W   T   E   C   S   K   S   C   D   G   G   T   Q   R   R   R   A   I
     Spacer Region                                                        TSP2

     =======================================================================
3421 TTCTGCCTGG ACTGAATGTT CAAAAAGCTG TGACGGTGGG ACCCAGAGGA GAAGGGCTAT
     AAGACGGACC TGACTTACAA GTTTTTCGAC ACTGCCACCC TGGGTCTCCT CTTCCCGATA


  +2    C   V   N   T   R   N   D   V   L   D   D   S   K   C   T   H   Q   E   K   V
                             TSP2

     =======================================================================
3481 TTGTGTCAAT ACCCGAAATG ATGTACTGGA TGACAGCAAA TGCACACATC AAGAGAAAGT
     AACACAGTTA TGGGCTTTAC TACATGACCT ACTGTCGTTT ACGTGTGTAG TTCTCTTTCA


  +2    T   I   Q   R   C   S   E   F   P   C   P   Q   W   K   S   G   D   W   S   E
     TSP2                                                                 TSP3

     ==================================================    =====================
3541 TACCATTCAG AGGTGCAGTG AGTTCCCTTG TCCACAGTGG AAATCTGGAG ACTGGTCAGA
     ATGGTAAGTC TCCACGTCAC TCAAGGGAAC AGGTGTCACC TTTAGACCTC TGACCAGTCT


  +2    C   L   V   T   C   G   K   G   H   K   H   R   Q   V   W   C   Q   F   G   E
                                                                 TSP3

     =======================================================================
3601 GTGCTTGGTC ACCTGTGGAA AAGGGCATAA GCACCGCCAG GTCTGGTGTC AGTTTGGTGA
     CACGAACCAG TGGACACCTT TTCCCGTATT CGTGGCGGTC CAGACCACAG TCAAACCACT


  +2    D   R   L   N   D   R   M   C   D   F   E   T   K   P   T   S   M   Q   T   C
     TSP3

     =======================================================================
3661 AGATCGATTA AATGATAGAA TGTGTGACCC TGAGACCAAG CCAACATCTA TGCAGACTTG
     TCTAGCTAAT TTACTATCTT ACACACTGGG ACTCTGGTTC GGTTGTAGAT ACGTCTGAAC


  +2    Q   Q   P   E   C   A   S   W   Q   A   G   P   W   G   Q   C   S   V   T   C
     TSP3                                                                 TSP4

     =================    ==================================================
3721 TCAGCAGCCG GAATGTGCAT CCTGGCAGGC GGGTCCCTGG GGACAGTGCA GTGTCACTTG
     AGTCGTCGGC CTTACACGTA GGACCGTCCG CCCAGGGACC CCTGTCACGT CACAGTGAAC
```

```
+2        G  Q  G    Y  Q  L  R    A  V  K    C  I  I    G  T  Y  M    S  V  V
                                                            TSP4

          =============================================================================
     3781 TGGACAGGGA TACCAGCTAA GAGCAGTGAA ATGCATCATT GGGACTTATA TGTCAGTGGT
          ACCTGTCCCT ATGGTCGATT CTCGTCACTT TACGTAGTAA CCCTGAATAT ACAGTCACCA


     +2      D  D  N    D  C  N  A    A  T  R    P  T  C    T  Q  D  C    E  L  F
          TSP4

          =============================================================================
     3841 AGATGACAAT GACTGTAATG CAGCAACTAG ACCAACTGAT ACCCAGGACT GTGAATTACC
          TCTACTGTTA CTGACATTAC GTCGTTGATC TGGTTGACTA TGGGTCCTGA CACTTAATGG


     +2      S  C  H    P  P  P  A    A  P  E    T  R  R    S  T  Y  S    A  P  R
          TSP4

          =======
     3901 ATCATGTCAT CCTCCCCCAG CTGCCCCGGA AACGAGGAGA AGCACATACA GTGCACCAAG
          TAGTACAGTA GGAGGGGGTC GACGGGGCCT TTGCTCCTCT TCGTGTATGT CACGTGGTTC


     +2      T  Q  W    R  F  G  S    W  T  P    C  S  A    T  C  G  K    G  T  R
                                                                           TSP5

          =============================================================================
     3961 AACCCAGTGG CGATTTGGGT CTTGGACCCC ATGCTCAGCC ACTTGTGGGA AAGGTACCCG
          TTGGGTCACC GCTAAACCCA GAACCTGGGG TACGAGTCGG TGAACACCCT TTCCATGGGC


     +2      M  R  Y    V  S  C  R    D  E  N    G  S  V    A  D  E  S    A  C  A
                        TSP5

          =============================================================================
     4021 GATGAGATAC GTCAGCTGCC GAGATGAGAA TGGCTCTGTG GCTGACGAGA GTGCCTGTGC
          CTACTCTATG CAGTCGACGG CTCTACTCTT ACCGAGACAC CGACTGCTCT CACGGACACG


     +2      T  L  P    R  P  V  A    K  E  E    C  S  V    T  P  C  G    Q  W  K
          TSP5                                                              TSP6

          =============================================================================
     4081 TACCCTGCCT AGACCAGTGG CAAAGGAAGA ATGTTCTGTG ACACCCTGTG GGCAATGGAA
          ATGGGACGGA TCTGGTCACC GTTTCCTTCT TACAAGACAC TGTGGGACAC CCGTTACCTT


     +2      A  L  D    W  S  S  C    S  V  T    C  G  Q    G  R  A  T    R  Q  V
                                                                           TSP6

          =============================================================================
     4141 GGCCTTGGAC TGGAGCTCTT GCTCTGTGAC CTGTGGGCAA GGTAGGGCAA CCCGGCAAGT
          CCGGAACCTG ACCTCGAGAA CGAGACACTG GACACCCGTT CCATCCCGTT GGGCCGTTCA


     +2      M  C  V    N  Y  S  D    H  V  I    D  R  S    E  C  D  Q    D  Y  I
                        TSP6

          =============================================================================
     4201 GATGTGTGTC AACTACAGTG ACCACGTGAT CGATCGGAGT GAGTGTGACC AGGATTATAT
          CTACACACAG TTGATGTCAC TGGTGCACTA GCTAGCCTCA CTCACACTGG TCCTAATATA


     +2      P  E  T    D  Q  D  C    S  M  S    P  C  P    Q  R  T  P    D  S  G
          TSP6

          ==============================================================
     4261 CCCAGAAACT GACCAGGACT GTTCCATGTC ACCATGCCCT CAAAGGACCC CAGACAGTGG
          GGGTCTTTGA CTGGTCCTGA CAAGGTACAG TGGTACGGGA GTTTCCTGGG GTCTGTCACC
```

```
      +2   L  A  Q   H  P  F  Q   N  E  D   Y  R  F   R  S  A  S   P  S  F
    4321  CTTAGCTCAG CACCCCTTCC AAAATGAGGA CTATCGTCCC CGGAGCGCCA GCCCCAGCCC
          GAATCGAGTC GTGGGGAAGG TTTTACTCCT GATAGCAGGG GCCTCGCGGT CGGGGTCGGC


      -2   T  H  V   L  G  G  N   Q  W  R   T  G  P   W  G  A  C   S  S  T
                                                                  TSP7

          ========================================================
    4381  CACCCATGTG CTCGGTGCAA ACCAGTGGAG AACTGGCCCC TGGGGAGCAT GTTCCAGTAC
          GTGGGTACAC GAGCCACCTT TGGTCACCTC TTGACCGGGG ACCCCTCGTA CAAGGTCATG


      +2   C  A  G   G  S  Q  R   R  V  V   V  C  Q   D  E  N  G   Y  T  A
                                           TSP7

          ========================================================
    4441  CTGTGCTGGC GGATCCCAGC GGCGTGTTGT TGTATGTCAG GATGAAAATG GATACACCGC
          GACACGACCG CCTAGGGTCG CCGCACAACA ACATACAGTC CTACTTTTAC CTATGTGGCG


      +2   N  D  C   V  E  R  I   K  P  D   E  Q  R   A  C  E  S   G  P  C
           TSP7

          ========================================================
    4501  AAACGACTGT GTGGAGAGAA TAAAACCTGA TGAGCAAAGA GCCTGTGAAT CCGGCCCTTG
          TTTGCTGACA CACCTCTCTT ATTTTGGACT ACTCGTTTCT CGGACACTTA GGCCGGGAAC


      +2   P  Q  W   A  Y  G  N   W  G  E   C  T  K   L  C  G  G   G  I  R
           TSP7                                                    TSP8
          ==  =======================================================
    4561  TCCTCAGTGG GCTTATGGCA ACTGGGGAGA GTGCACTAAG CTGTGTGGTG GAGGCATAAG
          AGGAGTCACC CGAATACCGT TGACCCCTCT CACGTGATTC GACACACCAC CTCCGTATTC


      +2   T  R  L   V  V  C  Q   R  S  N   G  E  R   F  P  D  L   S  C  E
                                  TSP8
          ========================================================
    4621  AACAAGACTG GTGGTCTGTC AGCGGTCCAA CGGTGAACGG TTTCCAGATT TGAGCTGTGA
          TTGTTCTGAC CACCAGACAG TCGCCAGGTT GCCACTTGCC AAAGGTCTAA ACTCGACACT


      +2   I  L  D   K  P  P  D   R  E  Q   C  N  T   H  A  C  P   H  D  A
           TSP8
          ========================================================
    4681  AATTCTTGAT AAACCTCCCG ATCGTGAGCA GTGTAACACA CATGCTTGTC CACACGACGC
          TTAAGAACTA TTTGGAGGGC TAGCACTCGT CACATTGTGT GTACGAACAG GTGTGCTGCG


      +2   A  W  S   T. G  P  W   S  S  C   S  V  S   C  G  R  G   H  K  Q
                                                                  TSP9

          ========================================================
    4741  TGCATGGAGT ACTGGCCCTT GGAGCTCGTG TTCTGTCTCT TGTGGTCGAG GGCATAAACA
          ACGTACCTCA TGACCGGGAA CCTCGAGCAC AAGACAGAGA ACACCAGCTC CCGTATTTGT


      +2   R  N  V   Y  C  M  A   K  D  G   S  H  L   E  S  D  Y   C  K  H
                                  TSP9
          ========================================================
    4801  ACGAAATGTT TACTGCATGG CAAAAGATGG AAGCCATTTA GAAAGTGATT ACTGTAAGCA
          TGCTTTACAA ATGACGTACC GTTTTCTACC TTCGGTAAAT CTTTCACTAA TGACATTCGT


      +2   L  A  K   P  H  G  H   R  K  C   R  G  G   R  C  P  K   W  K  A
           TSP9                                                    TSP10
```

```
      =======================================================        ========
4861  CCTGGCTAAG CCACATGGGC ACAGAAAGTG CCGAGGAGGA AGATGCCCCA AATGGAAAGC
      GGACCGATTC GGTGTACCCG TGTCTTTCAC GGCTCCTCCT TCTACGGGGT TTACCTTTCG

 +2    G  A  W   S  Q  C  S   V  S  C   G  R  G   V  Q  Q  R   H  V  G
                                                               TSP10
      =================================================================
4921  TGGCGCTTGG AGTCAGTGCT CTGTGTCCTG TGGCCGAGGC GTACAGCAGA GGCATGTGGG
      ACCGCGAACC TCAGTCACGA GACACAGGAC ACCGGCTCCG CATGTCGTCT CCGTACACCC

 +2    C  Q  I   G  T  H  K   I  A  R   E  T  E   C  N  P  Y   T  R  F
                 TSP10
      =================================================================
4981  CTGTCAGATC GGAACACACA AAATAGCCAG AGAGACCGAG TGCAACCCAT ACACCAGACC
      GACAGTCTAG CCTTGTGTGT TTTATCGGTC TCTCTGGCTC ACGTTGGGTA TGTGGTCTGG

 +2    E  S  E   R  D  C  Q   G  P  R   C  P  L   Y  T  W  R   A  E  E
       TSP10                                                   TSP11
      ===================================         =====
5041  GGAGTCGGAA CGCGACTGCC AAGGCCCACG GTGTCCCCTC TACACTTGGA GGGCAGAGGA
      CCTCAGCCTT GCGCTGACGG TTCCGGGTGC CACAGGGGAG ATGTGAACCT CCCGTCTCCT

 +2    W  Q  E   C  T  K  T   C  G  E   G  S  R   Y  R  K  V   V  C  V
                                                               TSP11
      =================================================================
5101  ATGGCAAGAA TGCACCAAGA CCTGCGGCGA AGGCTCCAGG TACCGCAAGG TGGTGTGTGT
      TACCGTTCTT ACGTGGTTCT GGACGCCGCT TCCGAGGTCC ATGGCGTTCC ACCACACACA

 +2    D  D  N   K  N  E  V   H  G  A   R  C  D   V  S  K  R   P  V  D
                 TSP11
      ==================================================================
5161  GGATGACAAC AAAAACGAGG TGCATGGGGC ACGCTGTGAC GTGAGCAAGC GGCCGGTGGA
      CCTACTGTTG TTTTTGCTCC ACGTACCCCG TGCGACACTG CACTCGTTCG CCGGCCACCT

 +2    R  E  S   C  S  L  Q   P  C  E   Y  V  W   I  T  G  E   W  S  E
       TSP11
      ==============================
5221  CCGTGAAAGC TGTAGTTTGC AACCCTGCGA GTATGTCTGG ATCACAGGAG AATGGTCAGA
      GGCACTTTCG ACATCAAACG TTGGGACGCT CATACAGACC TAGTGTCCTC TTACCAGTCT

 +2    V  P  S   W  E  L  *
                       ·Termination  codon
                              ====
5281  GGTACCGTCC TGGGAACTGT AACCATCGTC AGCTCAGCCA TGGCCTGAGA GTGGCAGAGG
      CCATGGCAGG ACCCTTGACA TTGGTAGCAG TCGAGTCGGT ACCGGACTCT CACCGTCTCC

5341  GATGAGTGGA GGGATGAGTG CAGGAATGTG GGAGACTTGA GGCTACCCGC CCGATTTGCC
      CTACTCACCT CCCTACTCAC GTCCTTACAC CCTCTGAACT CCGATGGGCG GGCTAAACGG

5401  ACTGTGAACT GTGTGTTTTC TGACAAGTCC TCAGCTTTCC CAAGCTAGAA TTCCTTGTAT
      TGACACTTGA CACACAAAAG ACTGTTCAGG AGTCGAAAGG GTTCGATCTT AAGGAACATA

5461  GCAAAGCGGG AGAGATGTAA GAGATGGTCT CTAAGTCCCT TCAGGTCTAC ATTCTGTGAT
      CGTTTCGCCC TCTCTACATT CTCTACCAGA GATTCAGGGA AGTCCAGATG TAAGACACTA
```

```
5521   TCACCTTGAT GTCCTATTGG CATAAAGAAG AAATTATTAC AGGGGCTGCA AACTCATAGG
       AGTGGAACTA CAGGATAACC GTATTTCTTC TTTAATAATG TCCCCGACGT TTGAGTATCC

5581   ATGCTGTGAG GTGCCTGAAG ACAGTTAAGT ATAAGAAAAT ATTGTAGTGC CAGGGATACA
       TACGACACTC CACGGACTTC TGTCAATTCA TATTCTTTTA TAACATCACG GTCCCTATGT

5641   ACAAGGAGAG ATGGCAACTG TGACAAACTA GCACATGCTG TGTGAAGGGA GCAGAATCTC
       TGTTCCTCTC TACCGTTGAC ACTGTTTGAT CGTGTACGAC ACACTTCCCT CGTCTTAGAG

5701   TTTCACTCCA GCTGTGGCCA TGCAGAAATG TGGTCTAGCG TTACCAGACC TGATTTTTCA
       AAAGTGAGGT CGACACCGGT ACGTCTTTAC ACCAGATCGC AATGGTCTGG ACTAAAAAGT

5761   AGAGAGGCTA AAAATCTGGA CTAGTATGTG AGATTTCCTA ACTTGAAAAT GGGGGCTGAA
       TCTCTCCGAT TTTTAGACCT GATCATACAC TCTAAAGGAT TGAACTTTTA CCCCCGACTT

5821   ATTTTTGGTT TTAAAACATT GTAAGGGGCA AACAAACCCC TTTCATGAAC CAGATGTGTT
       TAAAAACCAA AATTTTGTAA CATTCCCCGT TTGTTTGGGG AAAGTACTTG GTCTACACAA

5881   GTGCCTGTTT AACAAACAGC TTCAGAGGAA GAAAATAATT TTCTATAATA TCCGAAGTAT
       CACGGACAAA TTGTTTGTCG AAGTCTCCTT CTTTTATTAA AAGATATTAT AGGCTTCATA

5941   CTCAAGTACC ATTTTTTCAT ATATCTTCCT GTGCACAATG CTTATCTAGA CCCTTTTTAA
       GAGTTCATGG TAAAAAAGTA TATAGAAGGA CACGTGTTAC GAATAGATCT GGGAAAAATT

           PolyA Site
           ======
6001   TGGTAATAAA CCAGTAGTAA TCAT
       ACCATTATTT GGTCATCATT AGTA
```

Fig. 4

Metalloproteinase Domain Alignment of TS-SI v ADAMTS Family

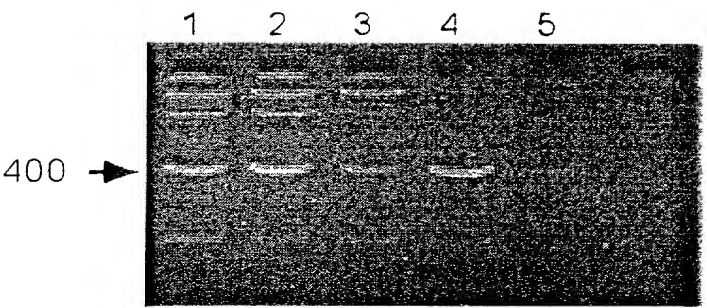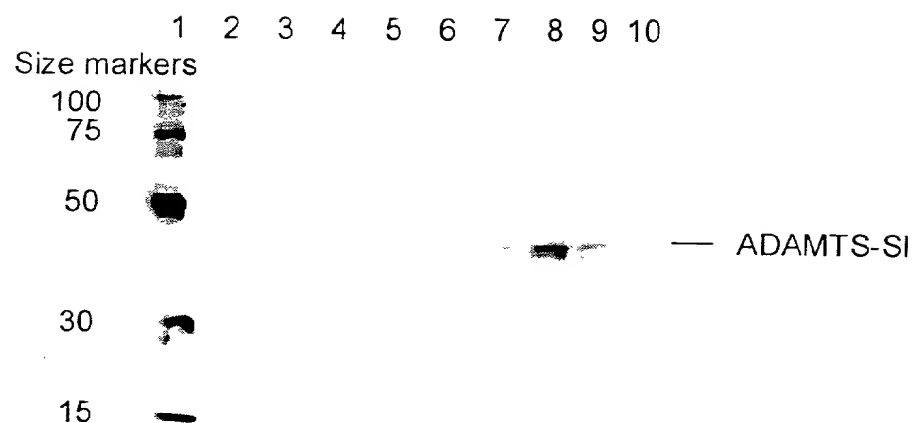| | | Percent Homology (SI vs) |
		Sim	Ident
hADAMTS-4	(AB014588)	62	46
hADAMTS-5	(AF142099)	58	44
hADAMTS-1	(AF060152)	63	50
hADAMTS-8	(AF060153)	62	49
hADAMTS-2	(AJ003125)	52	33

FIG 5

Figure 6

Lane 1 His Ladder (Qiagen)
Lane 2 Empty well
Lane 3 Total lysate
Lane 4 Unbound material
Lane 5 Wash material
Lane 6 50 mM Imidazole Eluate
Lane 7 100 mM Imidazole Eluate
Lane 8 250 mM Imidazole Eluate
Lane 9 2nd 250 mM Imidazole Eluate
Lane 10 Ni-NTA resin

FIG. 7

Mock Lysate
TS-SI Lysate
Ni-NTA purified - Mock
Ni-NTA purified - TS-SI

Unprocessed (180 kDa)
Processed (147 kDa)

191 kDa
97
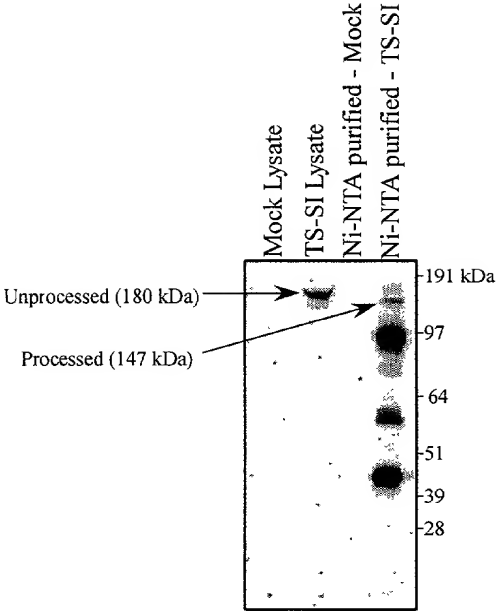64
51
39
28

FIG. 8

A   B

Lane   1   2   3   1   2

Western Blot analysis of ADAMTS-4 and ADAMTS-SI cleavage of aggrecanase substrate. A, lane 1 = uncleaved substrate, lane 2 = ADAMTS-4, lane 3 = ADAMTS-4 + 1 μM compound I.   B, lane 1 = ADAMTS-SI and lane 2 = ADAMTS-SI + 1 μM compound I.